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       Hanrahan, James Patrick
        Juengel, Jennifer Lee
       McNatty, Kenneth Pattrick
       Mulsant, Philippe
        Powell, Richard Patrick
<120> NEW GDF-9 AND GDF-9B (BMP-15) SEQUENCES FOR
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ctc ctt tcc Leu Leu Ser							346			
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cct aga gct cca tac tca ttt Pro Arg Ala Pro Tyr Ser Phe -125	acc tat aac to Thr Tyr Asn Se -120	ca cag ttt gaa er Gln Phe Glu -115	ttt 1056 Phe
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aac gac aca agt gct cag gct t Asn Asp Thr Ser Ala Gln Ala P -50 -45	tt cac agg tgg Phe His Arg Trp -40	cat tcc ctc cac His Ser Leu His	cct 1293 Pro -35
aaa agg aag cct tca cag ggt c Lys Arg Lys Pro Ser Gln Gly P -30	cct gac cag aag Pro Asp Gln Lys -25	aga ggg cta tct Arg Gly Leu Ser -20	' Ala
tac ccc gtg gga gaa gaa gct g Tyr Pro Val Gly Glu Glu Ala A -15	gct gag ggt gta la Glu Gly Val -10	aga tcg tcc cgt Arg Ser Ser Arg -5	cac 1389 His
cgc aga gac cag gag agt gcc a Arg Arg Asp Gln Glu Ser Ala S -1 1 5	agc tct gaa ttg Ser Ser Glu Leu	aag aag cct ctg Lys Lys Pro Leu 10	gtt 1437 Val
cca gct tca gtc aat ctg agt g Pro Ala Ser Val Asn Leu Ser G 15 20	gaa tac ttc aaa Glu Tyr Phe Lys 25	cag ttt ctt ttt Gln Phe Leu Phe	ccc 1485 Pro 30
cag aat gaa tgt gag ctc cat g Gln Asn Glu Cys Glu Leu His A 35	gac ttt aga ctt Asp Phe Arg Leu 40	agc ttt agt cag Ser Phe Ser Gln 45	
aag tgg gac aac tgg att gtg g Lys Trp Asp Asn Trp Ile Val A 50	gcc cca cac aaa Ala Pro His Lys 55	tac aac cct cga Tyr Asn Pro Arg 60	tac 1581 Tyr
tgt aaa ggg gac tgt ccc agg g Cys Lys Gly Asp Cys Pro Arg A	gcg gtc gga cat la Val Gly His	cgg tat ggc ttt Arg Tyr Gly Phe	ccg 1629 Pro

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-240

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-195 -185

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Glu His Leu Phe Lys Ser Val Leu Leu Tyr Thr Phe Asn Asn Ser -165 -160 -155

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-150 -145 -140

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-135 -130 -125

Ser Phe Thr Tyr Asn Ser Gln Phe Glu Phe Arg Lys Lys Tyr Lys -120 -115 -110

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-40 -35 -30

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-10 -5 -1 1

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His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile 40 45 50

Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro 55 60 65

Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln 70 75 80

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			cct Pro -255					ctg Leu -250	tat Tyr	gat Asp	ggg Gly	cac His	ggg Gly -245	gaa Glu	225
			ctg Leu -240					aga Arg -235							270
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			tat Tyr -120										tac Tyr -110	aaa Lys	630
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			aat a Asn I			let s					ir Cy				726

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ggc tca Gly Ser	atc Ile	gct Ala 120	tat Tyr	aaa Lys	gaa Glu	tat Tyr	gaa Glu 125	gat Asp	atg Met	ata Ile	gcc Ala	act Thr 130	aag Lys	tgt Cys	1350
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-300 -295 -290

Glu Ala Gln Ile Val Ala Arg Thr Ala Leu Glu Ser Glu Ala Glu
-285 -280 -275

Thr Trp Ser Leu Leu Asn His Leu Gly Gly Arg His Arg Pro Gly -270 -265 -260

Leu Leu Ser Pro Leu Leu Glu Val Leu Tyr Asp Gly His Gly Glu
-255 -250 -245

Pro Pro Arg Leu Gln Pro Asp Asp Arg Ala Leu Arg Tyr Met Lys -240 -235 -230

Arg Leu Tyr Lys Ala Tyr Ala Thr Lys Glu Gly Thr Pro Lys Ser -225 -220 -215

Asn Arg Arg His Leu Tyr Asn Thr Val Arg Leu Phe Thr Pro Cys
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Ala Gln His Lys Gln Ala Pro Gly Asp Leu Ala Ala Gly Thr Phe
-195 -185

Pro Ser Val Asp Leu Leu Phe Asn Leu Asp Arg Val Thr Val Val -180 -175 -170

Glu His Leu Phe Lys Ser Val Leu Leu Tyr Thr Phe Asn Asn Ser -165 -160 -155

Ile Ser Phe Pro Phe Pro Val Lys Cys Ile Cys Asn Leu Val Ile
-150 -145 -140

Lys Glu Pro Glu Phe Ser Ser Lys Thr Leu Pro Arg Ala Pro Tyr
-135 -130 -125

Ser Phe Thr Tyr Asn Ser Gln Phe Glu Phe Arg Lys Lys Tyr Lys Page 9 Trp Met Glu Ile Asp Val Thr Ala Pro Leu Glu Pro Leu Val Ala Ser -95 -105 -100

His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp

Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu -75 -65

Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln -60

Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln

Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu

Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
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Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu 20

Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu 25 30 35

His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile 45 40

Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro

Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
70 75 80

Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys 100 85

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Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr
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                                                      30
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Pro Ser Cys Val Pro Ala Lys Tyr 50

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70

				•			
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gtg agg ctg	gtg agg	ccg ctg	gct agt	gta gca	agg cct o	ctc aga g	577
Val Arg Leu 95	ı Val Arg	Pro Leu 100		val Ala	Arg Pro L 105	_eu Arg	
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tagaaaaaag	tggatctg	tc agttt	tctgt ca	ggcttcac	attgcctno	ca gtttgtactg	697
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cctcttacta		c tcc tally Ser T	gg cac a rp His I	le Gln Th	cc ctg gad nr Leu Asp 15	ttt cct ctg Phe Pro Leu 120	808
aga cca aac Arg Pro Asr	cgg gta Arg Val 125	Ala Tyr	caa cta Gln Leu	gtc aga Val Arg 130	gcc act g Ala Thr V	gtg gtt tac /al Val Tyr 135	856
cgc cat cag Arg His Glr	ctt cac Leu His 140	cta act Leu Thr	cat tcc His Ser 145	cac ctc His Leu	Ser Cys F	cat gtg gag His Val Glu L50	904
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						gag atg gat Glu Met Asp	1000
atc atg gaa Ile Met Glu 185	cat gtt His Val	ggg caa Gly Gln 190	aag ctc Lys Leu	tgg aat Trp Asn 195	cac aag g His Lys C	ggg cgc agg Gly Arg Arg 200	1048
gtt cta cga Val Leu Arg	ctc cgc Leu Arg 205	Phe Val	tgt cag Cys Gln	cag cca Gln Pro 210	aga ggt a Arg Gly S	agt gag gtt Ser Glu Val 215	1096
ctt gag tto Leu Glu Phe	tgg tgg Trp Trp 220	cat ggc His Gly	act tca Thr Ser 225	tca ttg Ser Leu	Asp Thr \	gtc ttc ttg /al Phe Leu 230	1144
tta ctg tat Leu Leu Tyr 235	Phe Asn			ttc agaa	gaccaa acc	ctctccct	1195
aaaggcctga	aagagttt	ac agaaa	aagac cc	ttctcttc	tcttgagga	ag ggctcgtcaa	1255
						gg gcctgaaagt	1315
						tg ggatcactgg	1375
				_	_	cc tcgggtacta	1435
_						ag tgagctggtg	1495
	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~					-5 -5-5-55-5	

## gatcagaatg tccctcagcc ttcctgtgtc ccttataagt atgttcccat tagcatcctt ctgattgagg caaatgggag tatcttgtac aaggagtatg agggtatgat tgcccagtcc tgcacatgca ggtgacggca aaggtgcagc tagctcaggt ttcccaagaa <210> <211> 239 <212> PRT <213> Ovis aries <220> <221> misc\_feature <222> (253)..(255) <223> atg start codon. <220> <221> misc\_feature <222> (1253)..(1255) <223> position of first codon of mature peptide in wildtype sheep. <220> <221> misc\_feature <222> (685)..() <223> n represents approx 5.2 kb of intron. <220> <221> misc\_feature <222> (1628)..(1630) <223> tga stop codon in wildtype sheep. <400> 8 Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile 20 Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu 35 45 40 Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln 115 Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His

Page 14

AJPARK27.001APC\_SEQUENCE LISTING.txt

1555

1615

130

Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr 145 150 155 160 Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu 165 170 175 Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys 180 190 Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys 20Ō 205 195 Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr 215 220 210 Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr 225 235 230 9 <210> <211> 1182 <212> DNA <213> Ovis areis <220> misc\_feature <221> <222> (1)..(3)<223> atg start codon <220> <221> mutation <222> (718)..(720)to t at 718 of [S1] sheep changes cag glutamine codon to tag STOP. <223> <220> <221> CDS <222> (1)..(717)<220> misc\_feature <221> <222> (805)..(807)<223> first codon of mature peptide in wildtype sheep. <220> <221> misc\_feature <222> (1180)..(1182) <223> tga stop codon. <400> 9 48 atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga ctg gtg ctt Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu 10 96 ttt atg gaa cat agg gtc caa atg aca cag gta ggg cag ccc tct att Phe Met Ğlu His Arg Val Gln Met Thr Gln Val Ğİy Gln Pro Ser Ile

Page 15

gcc cac ctg cct gag gcc cct acc ttg ccc ctg att cag gag ctg cta Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu 144

### AJPARK27.001APC\_SEQUENCE LISTING.txt gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg gtc tta ggg cat Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His ccc tta cgg tat atg ctg gag ctg tac cag cgt tca gct gac gca agt Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser gga cac cct agg gaa aac cgc acc att ggg gcc acc atg gtg agg ctg Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu gtg agg ccg ctg gct agt gta gca agg cct ctc aga ggc tcc tgg cac Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His ata cag acc ctg gac ttt cct ctg aga cca aac cgg gta gca tac caa Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln · cta gtc aga gcc act gtg gtt tac cgc cat cag ctt cac cta act cat Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His tcc cac ctc tcc tgc cat gtg gag ccc tgg gtc cag aaa agc cca acc Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr aat cac ttt cct tct tca gga aga ggc tcc tca aag cct tcc ctg ttg Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu ccc aaa act tgg aca gag atg gat atc atg gaa cat gtt ggg caa aag Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys ctc tgg aat cac aag ggg cgc agg gtt cta cga ctc cgc ttc gtg tgt Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys cag cag cca aga ggt agt gag gtt ctt gag ttc tgg tgg cat ggc act Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr tca tca ttg gac act gtc ttc ttg tta ctg tat ttc aat gac act Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr tagagtgttc agaagaccaa acctctccct aaaggcctga aagagtttac agaaaaagac ccttctcttc tcttgaggag ggctcgtcaa gcaggcagta ttgcatcgga agttcctggc ccctccaggg agcatgatgg gcctgaaagt aaccagtgtt ccctccaccc ttttcaagtc agcttccagc agctgggctg ggatcactgg atcattgctc cccatctcta taccccaaac tactgtaagg gagtatgtcc tcgggtacta cactatggtc tcaattctcc caatcatgcc

atcatccaga accttgtcag tgagctggtg gatcagaatg tccctcagcc ttcctgtgtc

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Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr Page 17

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gta gca agg cct ctc aga g gtgagttatc atactatatt gttctggtgg Val Ala Arg Pro Leu Arg -165	607
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caggetteae attgeetnea gtttgtaetg ageaggtetg ttagagagae taaggetagg	727
atataagaag ctaacgcttt gctcttgttc cctcttacta atgcag gc tcc tgg Gly Ser Trp -160	781
cac ata cag acc ctg gac ttt cct ctg aga cca aac cgg gta gca	826
His Ile Gln , Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala -155 -150 -145	
tac caa cta gtc aga gcc act gtg gtt tac cgc cat cag ctt cac Tyr Gln Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His -140 -135 -130	871
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ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt ctt gag ttc Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe -65 -60 -55 -50	1105
tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg tta ctg tat Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr -45 -40 -35	1153
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Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser Leu Leu Leu Arg Arg Ala
                            -10
                                                                     1297
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Arg Gln Ala Gly Ser Ile Ala Ser Glu Val Pro Gly Pro Ser Arg Glu
                                        10
                                                             15
                                                                     1345
cat gat ggg cct gaa agt aac cag tgt tcc ctc cac cct ttt caa gtc
His Asp Gly Pro Glu Ser Asn Gln Cys Ser Leu His Pro Phe Gln Val
                                                         30
                20
                                    25
                                                                     1393
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Ser Phe Gln Gln Leu Gly Trp Asp His Trp Ile Ile Ala Pro His Leu
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                                            75
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Leu Val Asp Gln Asn Val Pro Gln Pro Ser Cys Val Pro Tyr Lys Tyr
80
                    85
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Val Pro Ile Ile Leu Leu Ile Glu Ala Asn Gly Ser Ile Leu Tyr
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                                                         110
                100
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-235 -230 -225

Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg -220 -215 -210

Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg
-205 -200 -195

Ser Ala Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly
-190 -185 -180

Ala Thr Met Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg
-175 -170 -165

Pro Leu Arg Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu
-160 -155 -150

Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val -145 -140 -135

Tyr Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His
-130 -125 -120

Val Glu Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser -115 -110 -105

Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr -100 -95 -90

Glu Met Asp Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys -85 -80 -75

Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly
-70 -65 -60

Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr
-55 -45 -40

Val Phe Leu Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr
-35 -30 -25

Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser Page 22 Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val
-5 -1 1 5

Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser 10 20 25

Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp 30 40

Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
45 50 55

Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile 60 65 70

Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser

75 80 85

Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala 90 95 100 105

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isoleucine codon
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			acc ttg ccc cte Thr Leu Pro Le		35
gag ctg cta	gaa gaa gcc	cct ggc aag	cag cag agg aa	g ccg cgg 18	30
Glu Leu Leu	Glu Glu Ala -220	Pro Gly Lys -215	Gln Gln Arg Ly	s Pro Arg -210	
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aga cca aac Arg Pro Asn	cgg gta gca Arg Val Ala -145	tac caa cta Tyr Gln Leu -140	gtc aga gcc ac Val Arg Ala Th	t gtg gtt 40 r Val Val -135	)5
tac cgc cat Tyr Arg His	cag ctt cac Gln Leu His -130	cta act cat Leu Thr His -125	tcc cac ctc tc Ser His Leu Se	c tgc cat 45 r Cys His -120	50
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tca gga aga Ser Gly Arg	ggc tcc tca Gly Ser Ser -100	aag cct tcc o Lys Pro Ser I -95	ctg ttg ccc aaa Leu Leu Pro Lys	act tgg aca 54 Thr Trp Thr -90	13
			aa aag ctc tgg In Lys Leu Trp -75		<b>)</b> 1
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                                                                      927
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                                    35
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Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
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    75
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                                         100
                                                                     1167
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Asn Ğİğ Ser Ile Leŭ Tyr Lys Ğlū Tyr Ğlū Ğİy Met Ile Ala Gln Ser
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-250 -245 -240

Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln
-235 -230 -225

Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg
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Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg -205 -200 -195

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-130 -125 -120

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-70 -65 -60

Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr
-55 -45 -40

Val Phe Leu Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr
-35 -30 -25

Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser -20 -15 -10

Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val

Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
45 50 55 Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala 105 Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser 110 Cys Thr Cys Arg 125 <210> 168 DNA <213> Ovis aries <220> <221> CDS (1)..(168)<222> <220> <221> mutation <222> (85)..(87) <223> g to t at 86 of GDF9B sheep changes agc serine codon to atc isoleucine codon <400> 17 48 gcc atc atc cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro 10 96 cag cct tcc tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Leu Leu 144 att gag gca aat ggg agt atc ttg tac aag gag tat gag ggt atg att Ile Ğlū Āla Asn Ğly Ser Ile Leu Tyr Lys Ğlü Tyr Ğlü Ğly Met Ile Page 27

gcc cag tcc tgc aca tgc agg tga Ala Gln Ser Cys Thr Cys Arg 50 55 168

<210> 18

<211> 55

<212> PRT

<213> Ovis aries

<400> 18

Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro 1 10 15

Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Leu Leu 20 25 30

Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile 35 40 45

Ala Gln Ser Cys Thr Cys Arg 50 55